In the Specification:

Please amend the specification as shown:

Please delete paragraph [00150] and replace it with the following paragraph:

[00150] Human ENaC cDNAs for α, β and γ ENaC were amplified from human kidney cDNA (Origene Technologies Inc.) by PCR using the following primer pairs, respectively: 5' CGC GGA TCC GCC CAT ACC AGG TCT CAT G 3' **(SEQ ID NO: 9)** and 5' CCG GAA TTC CTG CAC ATC CTT CAA TCT TGC 3' **(SEQ ID NO: 10)**; 5' CGC GGA TCC AGC AGG TGC CAC TAT GCA C 3' **(SEQ ID NO: 11)** and CCG CTC GAG GTC TTG GCT GCT CAG TGA G 3' **(SEQ ID NO: 12)**; 5' CGC GGA TCC CCT CAA AGT CCC ATC CTC G 3' **(SEQ ID NO: 13)** and 5' CCG GAA TTC GAC TAG ATC TGT CTT CTC AAC 3' **(SEQ ID NO: 14)**. The primers were designed to be complementary to 5' and 3'-untranslated region sequence in order to retain the endogenous translation initiation signal, and they introduced terminal restriction endonuclease sites that were used to clone amplified ENaC cDNAs into the mammalian expression vector pcDNA3 (Invitrogen) for functional expression experiments. The cloned ENaC cDNAs were sequenced and compared to ENaC sequences in public DNA databanks. Each cloned subunit is a composite of polymorphisms present in different databank alleles; that is, every polymorphism in each cloned subunit identified by pairwise comparison of the cloned subunit to a databank allele could be found in another databank allele. In addition, polymorphisms in cloned ENaC subunits were verified by sequencing of cloned cDNAs amplified in independent PCR experiments.